Amendments to the Specification:

Please replace tables A-1 and A-2, at page 62 with the following amended tables:

Table A-1: Phage isolated with Abl SH3 domain data

Library	Strong Binding >1.75 OD	Weak Binding 0.5-1.74 OD	non-specific <0.5 OD
Random X_{12}	0	10	2
X_5FX_5	0	0	12
X_5DX_5	0	2	10
X_5RX_5	2	4	6
X_5PX_5	7	0	5
$X_6PXPPXPX_2$ (Class I SH3) **(SEQ ID NO:14)**	7	3	2

Table A-2: Phage isolated with the Src SH3 domain

Library	Strong Binding >1.75 OD	Weak Binding 0.5-1.74 OD	non-specific <0.5 OD
Random X_{12}	3	0	2
X_5FX_5	1	1	3
X_5DX_5	4	1	0
X_5RX_5	0	0	5
X_5PX_5	4	1	0
$X_6PXPPXPX_2$ (Class I SH3) **(SEQ ID NO:14)**	3	0	2

Please replace the paragraph beginning at page 92, line 33 with the following amended paragraph:

Frequency	Sequence
8	G K G W K C F G A L C (SEQ ID NO:32)
2	S T T F Q C V G L L C (SEQ ID NO:33)
1	A N G W E C I G Q F C (SEQ ID NO:34)
1	K P V W K C T G L F C (SEQ ID NO:35)
1	S A Q W Q C V G E F C (SEQ ID NO:36)
1 Consensus	W Phi C Pho G x F/L C **(SEQ ID NO:169)**

Phi=hydrophilic
Pho=hydrophobic

2	L	P	M	A	R	W	T	C	V	N	C (SEQ ID NO:37)
1	A	V	D	R	G	W	T	C	V	N	C (SEQ ID NO:38)
1	Q	I	T	P	Q	W	T	C	I	N	C (SEQ ID NO:39)
1 Consensus						W	T	C	V/I	N	C **(SEQ ID NO:170)**

1	G	V	C	Q	S	S	D	H	R	E	C (SEQ ID NO:40)
1	G	W	Q	E	R	F	Q	Q	E	D	R (SEQ ID NO:41)
1	E	V	P	T	T	K	V	L	W	P	S (SEQ ID NO:42)

Please replace the paragraph beginning at page 95, line 35 with the following amended paragraph:

Enrichment for binders monitored by pool ELISA. After 3 rounds of selection, the only libraries which showed an enrichment for binding phage were the H and W libraries. 95 clones were tested, 48 from the H library and 47 from the W library. Strong binding was observed on 5 from the H library and 28 from the W library. Testing the specificity of these 33 phage against a variety of proteins showed that 17 of them bound to give strong signals and were very specific. The ~~DNA~~ AA sequences for the displayed phage were determined and are shown below:

Please replace the paragraph beginning at page 96, line 20 with the following amended paragraph:

These peptides sequences can be placed in two groups. The first group align between themselves to form the consensus sequence FxDyWqdL (AAs 2-9 of SEQ ID NO:47) where the upper case residues are completely conserved. This sequence aligns perfectly with a sequence with the human or mouse p53 protein that has been shown to interact with the N terminal portion of hMDM2 by biochemical studies and crystallography (Leng et al 1995 and Kussie et al 1996). The other peptides have limited homology to each other and do not align with peptide sequences from p53 or any other protein in genbank.

Please replace the paragraph beginning at page 139, line 12 with the following amended paragraph:

Ex	Target	Peptide
1	HCMV UL44	E-H-V-C-S-W-G-W-G-R-C ~~(SEQ ID NO:168)~~ D R L T K ~~(SEQ ID NO:169)~~ N K I A H ~~(SEQ ID NO:170)~~ Q M G ~~(SEQ ID NO:171)~~ (SEQ ID NO:168)
2	Protein Kinase CβII	W-Phi-C-Pho-G-X-(F/L)-C (SEQ ID NO:169) and W-T-C-(V/I)-N- C (SEQ ID NO:170)
3	human MDM2	S-F-T-D-Y-W-R-D-L-E-Q (SEQ ID NO:~~172~~ 171) and conservative mutants thereof.
5	~~tyrosine Trna~~ TyrRS	Y-Phi-W-P-W (SEQ ID NO:179) and Y-Phi-W-P-Phi and (Y/F)-(S/T/G/A/H)-W-P(W/G/D/S/P) and (Y/F/W/L)-W-W-P-(D/E/S/N)-W-G (SEQ ID NO:172)
8	glucosidase	{F-K}-P-W-P-(I/V)-Y (SEQ ID NO:173) {}=optional

carboxypeptidase P-G-W-W (SEQ ID NO:~~173~~ 180)

ProRS S-R-D-W-G-F-W ~~(SEQ ID NO:174)~~
E (SEQ ID NO:~~175~~ 174)

11 Estrogen Receptor W-Pho-R-L-Phi-D-Pho-P-W-G (SEQ ID NO:175) and
C-F-F-W-D (SEQ ID NO:176) and
L-X-X-L-L (SEQ ID NO:177)